

- Added an option to `package.dependencies()` to handle the 'Suggests' levels of dependencies.
 - Vignette dependencies can now be checked and obtained via `vignetteDepends`.
 - Option "repositories" to list URLs for package repositories added.
 - `package.description()` has been replaced by `packageDescription()`.
 - R CMD INSTALL/build now skip Subversion's `.svn` directories as well as CVS directories.
 - `arraySubscript` and `vectorSubscript` take a new argument which is a function pointer that provides access to character strings (such as the names vector) rather than assuming these are passed in.
 - `R_CheckUserInterrupt` is now described in 'Writing R Extensions' and there is a new equivalent subroutine `rchkusr` for calling from FORTRAN code.
 - `hsv2rgb` and `rgb2hsv` are newly in the C API.
 - `Salloc` and `Srealloc` are provided in `S.h` as wrappers for `S_alloc` and `S_realloc`, since current `S` versions use these forms.
 - The type used for vector lengths is now `R_len_t` rather than `int`, to allow for a future change.
 - The internal header `nmath/dpq.h` has slightly improved macros `R_DT_val()` and `R_DT_Cval()`, a new `R_D_LExp()` and improved `R_DT_log()` and `R_DT_Clog()`; this improves accuracy in several `[dpq]`-functions for extreme arguments.
 - `print.coefmat()` is defunct, replaced by `printCoefmat()`.
 - `codes()` and `codes<-()` are defunct.
 - `anovalist.lm` (replaced in 1.2.0) is now defunct.
 - `glm.fit.null()`, `lm.fit.null()` and `lm.wfit.null()` are defunct.
 - `print.atomic()` is defunct.
 - The command-line arguments `--nsize` and `--vsize` are no longer recognized as synonyms for `--min-nsize` and `--min-vsize` (which replaced them in 1.2.0).
 - Unnecessary methods `{coef.{g}lm}` and `fitted.{g}lm` have been removed: they were each identical to the default method.
 - `La.eigen()` is deprecated now `eigen()` uses LAPACK by default.
 - `tetragamma()` and `pentagamma()` are deprecated, since they are equivalent to `psigamma(, deriv=2)` and `psigamma(, deriv=3)`.
 - `LTRUE/LFALSE` in `Rmath.h` have been removed: they were deprecated in 1.2.0.
 - `package.contents()` and `package.description()` have been deprecated.
 - The defaults for `configure` are now `--without-zlib--without-bzlib--without-pcre`. The included PCRE sources have been updated to version 4.5 and PCRE ≥ 4.0 is now required if `--with-pcre` is used. The included zlib sources have been updated to 1.2.1, and this is now required if `--with-zlib` is used.
 - `configure` no longer lists `bzip2` and PCRE as 'additional capabilities' as all builds of R have had them since 1.7.0.
 - `--with-blasgoto=` to use K. Goto's optimized BLAS will now work.
- The above lists only new features, see the 'NEWS' file in the R distribution or on the R homepage for a list of bug fixes.

Changes on CRAN

by Kurt Hornik

New contributed packages

AlgDesign Algorithmic experimental designs. Calculates exact and approximate theory experimental designs for D, A, and I criteria. Very large designs may be created. Experimental de-

signs may be blocked or blocked designs created from a candidate list, using several criteria. The blocking can be done when whole and within plot factors interact. By Bob Wheeler.

BradleyTerry Specify and fit the Bradley-Terry model and structured versions. By David Firth.

BsMD Bayes screening and model discrimination

follow-up designs. By Ernesto Barrios based on Daniel Meyer's code.

DCluster A set of functions for the detection of spatial clusters of disease using count data. Bootstrap is used to estimate sampling distributions of statistics. By Virgilio Gómez-Rubio, Juan Ferrándiz, Antonio López.

GeneTS A package for analyzing multiple gene expression time series data. Currently, **GeneTS** implements methods for cell cycle analysis and for inferring large sparse graphical Gaussian models. For plotting the inferred genetic networks **GeneTS** requires the **graph** and **Rgraphviz** packages (available from www.bioconductor.org). By Konstantinos Fokianos, Juliane Schaefer, and Korbinian Strimmer.

HighProbability Provides a simple, fast, reliable solution to the multiple testing problem. Given a vector of p -values or achieved significance levels computed using standard frequentist inference, **HighProbability** determines which ones are low enough that their alternative hypotheses can be considered highly probable. The p -value vector may be determined using existing R functions such as `t.test`, `wilcox.test`, `cor.test`, or `sample`. **HighProbability** can be used to detect differential gene expression and to solve other problems involving a large number of hypothesis tests. By David R. Bickel.

Icens Many functions for computing the NPMLE for censored and truncated data. By R. Gentleman and Alain Vandal.

MCMCpack This package contains functions for posterior simulation for a number of statistical models. All simulation is done in compiled C++ written in the Scythe Statistical Library Version 0.4. All models return coda mcmc objects that can then be summarized using coda functions or the coda menu interface. The package also contains some useful utility functions, including some additional PDFs and pseudo-random number generators for statistical distributions. By Andrew D. Martin, and Kevin M. Quinn.

MNP A publicly available R package that fits the Bayesian Multinomial Probit models via Markov chain Monte Carlo. Along with the standard Multinomial Probit model, it can also fit models with different choice sets for each observation and complete or partial ordering of all the available alternatives. The estimation is based on the efficient marginal data augmentation algorithm that is developed by Imai and van Dyk (2004). By Kosuke Imai, Jordan Vance, David A. van Dyk.

NADA Contains methods described by Dennis R. Helsel in his book "Nondetects And Data Analysis: Statistics for Censored Environmental Data". By Lopaka Lee.

R2WinBUGS Using this package, it is possible to call a BUGS model, summarize inferences and convergence in a table and graph, and save the simulations in arrays for easy access in R. By originally written by Andrew Gelman; changes and packaged by Sibylle Sturtz and Uwe Ligges.

RScalAPACK An interface to ScaLAPACK functions from R. By Nagiza F. Samatova, Srikanth Yoginath, and David Bauer.

RUnit R functions implementing a standard Unit Testing framework, with additional code inspection and report generation tools. By Matthias Burger, Klaus Juenemann, Thomas Koenig.

SIN This package provides routines to perform SIN model selection as described in Drton & Perlman (2004). The selected models are in the format of the **ggm** package, which allows in particular parameter estimation in the selected model. By Mathias Drton.

SoPhy SWMS_2D interface, Submission to Computers and Geosciences, title: The use of the language interface of R: two examples for modelling water flux and solute transport. By Martin Schlather, Bernd Huwe.

SparseLogReg Some functions wrapping the sparse logistic regression code by S. K. Shevade and S. S. Keerthi originally intended for microarray-based gene selection. By Michael T. Mader, with C code from S. K. Shevade and S. S. Keerthi.

assist ASSIST, see manual. By Yuedong Wang, and Chunlei Ke.

bayesmix Bayesian mixture models of univariate Gaussian distributions using JAGS. By Bettina Gruen.

betareg Beta regression for modeling rates and proportions. By Alexandre de Bustamante Simas.

circular Circular Statistics, from "Topics in circular Statistics" (2001) S. Rao Jammalamadaka and A. SenGupta, World Scientific. By Ulric Lund, Claudio Agostinelli.

crossdes Contains functions for the construction and randomization of balanced carryover balanced designs. Contains functions to check

given designs for balance. Also contains functions for simulation studies on the validity of two randomization procedures. By Martin Oliver Sailer.

debug Debugger for R functions, with code display, graceful error recovery, line-numbered conditional breakpoints, access to exit code, flow control, and full keyboard input. By Mark V. Bravington.

distr Object orientated implementation of distributions and some additional functionality. By Florian Camphausen, Matthias Kohl, Peter Ruckdeschel, Thomas Stabla.

dynamicGraph Interactive graphical tool for manipulating graphs. By Jens Henrik Badsberg.

energy E-statistics (energy) tests for comparing distributions: multivariate normality, Poisson test, multivariate k -sample test for equal distributions, hierarchical clustering by e-distances. Energy-statistics concept based on a generalization of Newton's potential energy is due to Gabor J. Szekely. By Maria L. Rizzo and Gabor J. Szekely.

evdbayes Provides functions for the bayesian analysis of extreme value models, using MCMC methods. By Alec Stephenson.

evir Functions for extreme value theory, which may be divided into the following groups; exploratory data analysis, block maxima, peaks over thresholds (univariate and bivariate), point processes, gev/gpd distributions. By S original (EVIS) by Alexander McNeil, R port by Alec Stephenson.

fBasics fBasics package from Rmetrics — Rmetrics is an Environment and Software Collection for teaching "Financial Engineering and Computational Finance". By Diethelm Wuertz and many others, see the SOURCE file.

fExtremes fExtremes package from Rmetrics. By Diethelm Wuertz and many others, see the SOURCE file.

fOptions fOptions package from Rmetrics. By Diethelm Wuertz and many others, see the SOURCE file.

fSeries fOptions package from Rmetrics. By Diethelm Wuertz and many others, see the SOURCE file.

fortunes R Fortunes. By Achim Zeileis, fortune contributions from Torsten Hothorn, Peter Dalgaard, Uwe Ligges, Kevin Wright.

gap This is an integrated package for genetic data analysis of both population and family data. Currently it contains functions for sample size calculations of both population-based and family-based designs, probability of familial disease aggregation, kinship calculation, some statistics in linkage analysis, and association analysis involving one or more genetic markers including haplotype analysis. In the future it will incorporate programs for path and segregation analyses, as well as other statistics in linkage and association analyses. By Jing hua Zhao in collaboration with other colleagues, and with help from Kurt Hornik and Brian Ripley of the R core development team.

gclus Orders panels in scatterplot matrices and parallel coordinate displays by some merit index. Package contains various indices of merit, ordering functions, and enhanced versions of pairs and parcoord which color panels according to their merit level. By Catherine Hurley.

gpls Classification using generalized partial least squares for two-group and multi-group (more than 2 group) classification. By Beiying Ding.

hapassoc The following R functions are used for likelihood inference of trait associations with haplotypes and other covariates in generalized linear models. The functions accommodate uncertain haplotype phase and can handle missing genotypes at some SNPs. By K. Burkett, B. McNeney, J. Graham.

haplo.stats Haplo Stats is a suite of S-PLUS/R routines for the analysis of indirectly measured haplotypes. The statistical methods assume that all subjects are unrelated and that haplotypes are ambiguous (due to unknown linkage phase of the genetic markers). The genetic markers are assumed to be codominant (i.e., one-to-one correspondence between their genotypes and their phenotypes), and so we refer to the measurements of genetic markers as genotypes. The main functions in Haplo Stats are: `haplo.em`, `haplo.glm` and `haplo.score`. By Jason P. Sinnwell and Daniel J. Schaid.

hett Functions for the fitting and summarizing of heteroscedastic t -regression. By Julian Taylor.

HttpRequest HTTP Request protocols. Implements the GET, POST and multipart POST request. By Eryk Witold Wolski.

impute Imputation for microarray data (currently KNN only). By Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, Gilbert Chu.

- kernlab** Kernel-based machine learning methods including support vector machines. By Alexandros Karatzoglou, Alex Smola, Achim Zeileis, Kurt Hornik.
- klaR** Miscellaneous functions for classification and visualization developed at the Department of Statistics, University of Dortmund. By Christian Röver, Nils Raabe, Karsten Luebke, Uwe Ligges.
- knncat** This program scales categorical variables in such a way as to make NN classification as accurate as possible. It also handles continuous variables and prior probabilities, and does intelligent variable selection and estimation of error rates and the right number of NN's. By Sam Buttrey.
- kza** Kolmogorov-Zurbenko Adaptive filter for locating change points in a time series. By Brian Close with contributions from Igor Zurbenko.
- mAr** Estimation of multivariate AR models through a computationally-efficient stepwise least-squares algorithm (Neumaier and Schneider, 2001); the procedure is of particular interest for high-dimensional data without missing values such as geophysical fields. By S. M. Barbosa.
- mathgraph** Simple tools for constructing and manipulating objects of class `mathgraph` from the book "S Poetry", available at <http://www.burns-stat.com/pages/spoetry.html>. By Original S code by Patrick J. Burns. Ported to R by Nick Efthymiou.
- mcgibbsit** Provides an implementation of Warnes & Raftery's MCGibbsit run-length diagnostic for a set of (not-necessarily independent) MCMC samplers. It combines the estimate error-bounding approach of Raftery and Lewis with evaluate between verses within chain approach of Gelman and Rubin. By Gregory R. Warnes.
- mixreg** Fits mixtures of one-variable regressions (which has been described as doing ANCOVA when you don't know the levels). By Rolf Turner.
- mscalib** Calibration and filtering methods for calibration of mass spectrometric peptide mass lists. Includes methods for internal, external calibration of mass lists. Provides methods for filtering chemical noise and peptide contaminants. By Eryk Witold Wolski.
- multinomRob** overdispersed multinomial regression using robust (LQD and tanh) estimation. By Walter R. Mebane, Jr., Jasjeet Singh Sekhon.
- mvbutils** Utilities for project organization, editing and backup, sourcing, documentation (formal and informal), package preparation, macro functions, and miscellaneous utilities. Needed by **debug** package. By Mark V. Bravington.
- mvpart** Multivariate regression trees. Original **rpart** by Terry M Therneau and Beth Atkinson, R port by Brian Ripley. Some routines from **vegan** by Jari Oksanen Extensions and adaptations of **rpart** to **mvpart** by Glenn De'ath.
- pgam** This work is aimed at extending a class of state space models for Poisson count data, so called Poisson-Gamma models, towards a semiparametric specification. Just like the generalized additive models (GAM), cubic splines are used for covariate smoothing. The semiparametric models are fitted by an iterative process that combines maximization of likelihood and backfitting algorithm. By Washington Junger.
- qcc** Shewhart quality control charts for continuous, attribute and count data. Cusum and EWMA charts. Operating characteristic curves. Process capability analysis. Pareto chart and cause-and-effect chart. By Luca Scrucca.
- race** Implementation of some racing methods for the empirical selection of the best. If the R package **rpvm** is installed (and if PVM is available, properly configured, and initialized), the evaluation of the candidates are performed in parallel on different hosts. By Mauro Birattari.
- rbugs** Functions to prepare files needed for running BUGS in batch-mode, and running BUGS from R. Support for Linux systems with Wine is emphasized. By Jun Yan (with part of the code modified from 'bugs.R', <http://www.stat.columbia.edu/~gelman/bugsR/>), by Andrew Gelman).
- ref** small package with functions for creating references, reading from and writing ro references and a memory efficient `refdata` type that transparently encapsulates matrixes and `data.frames`. By Jens Oehlschlägel.
- regress** Functions to fit Gaussian linear model by maximizing the residual log likelihood. The covariance structure can be written as a linear combination of known matrices. Can be used for multivariate models and random effects models. Easy straight forward manner to specify random effects models, including random interactions. By David Clifford, Peter McCullagh.
- rgl** 3D visualization device (OpenGL). By Daniel Adler.

- rlecuyer** Provides an interface to the C implementation of the random number generator with multiple independent streams developed by L'Ecuyer et al (2002). The main purpose of this package is to enable the use of this random number generator in parallel R applications. By Hana Sevcikova, Tony Rossini.
- rpart.permutation** Performs permutation tests of **rpart** models. By Daniel S. Myers.
- rrcov** Functions for Robust Location and Scatter Estimation and Robust Regression with High Breakdown Point (`covMcd()`, `ltsReg()`). Originally written for S-PLUS (`fastlts` and `fastmcd`) by Peter Rousseeuw & Katrien van Driessen, ported to R, adapted and packaged by Valentin Todorov.
- sandwich** Model-robust standard error estimators for time series and longitudinal data. By Thomas Lumley, Achim Zeileis.
- seqmon** A program that computes the probability of crossing sequential boundaries in a clinical trial. It implements the Armitage-McPherson and Rowe Algorithm using the method described in Schoenfeld D. (2001) "A simple Algorithm for Designing Group Sequential Clinical Trials", *Biometrics* 27, 972-974. By David A. Schoenfeld.
- setRNG** Set reproducible random number generator in R and S. By Paul Gilbert.
- sfsmisc** Useful utilities ['goodies'] from Seminar fuer Statistik ETH Zurich, many ported from S-plus times. By Martin Maechler and many others.
- skewt** Density, distribution function, quantile function and random generation for the skewed t distribution of Fernandez and Steel. By Robert King,, with contributions from Emily Anderson.
- spatialCovariance** Functions that compute the spatial covariance matrix for the matern and power classes of spatial models, for data that arise on rectangular units. This code can also be used for the change of support problem and for spatial data that arise on irregularly shaped regions like counties or zipcodes by laying a fine grid of rectangles and aggregating the integrals in a form of Riemann integration. By David Clifford.
- spc** Evaluation of control charts by means of the zero-state, steady-state ARL (Average Run Length). Setting up control charts for given in-control ARL and plotting of the related figures. The control charts under consideration are one- and two-sided EWMA and CUSUM charts for monitoring the mean of normally distributed independent data. Other charts and parameters are in preparation. Further SPC areas will be covered as well (sampling plans, capability indices, ...). By Sven Knoth.
- spe** Implements stochastic proximity embedding as described by Agrafiotis et al. in PNAS, 2002, 99, pg 15869 and J. Comput. Chem., 2003,24, pg 1215. By Rajarshi Guha.
- supclust** Methodology for Supervised Grouping of Predictor Variables. By Marcel Dettling and Martin Maechler.
- svmpath** Computes the entire regularization path for the two-class SVM classifier with essentially the same cost as a single SVM fit. By Trevor Hastie.
- treeglia** Stem analysis functions for volume increment and carbon uptake assessment from tree-rings. By Marco Bascietto.
- urca** Unit root and cointegration tests encountered in applied econometric analysis are implemented. By Bernhard Pfaff.
- urn** Functions for sampling without replacement. (Simulated Urns). By Micah Altman.
- verify** This small package contains simple tools for constructing and manipulating objects of class `verify`. These are used when regression-testing R software. By S Original by Patrick J. Burns. Ported to R by Nick Efthymiou.
- zoo** A class with methods for totally ordered indexed observations such as irregular time series. By Achim Zeileis, Gabor Grothendieck.

Other changes

- Packages **mclust1998**, **netCDF**, and **serialize** were moved from the main CRAN section to the Archive.

Kurt Hornik
 Wirtschaftsuniversität Wien, Austria
Kurt.Hornik@R-project.org